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Table 1. Multidimensional NMR experiments							
Experiment (acquisition of central peaks)*	Indirect † dimension(s)	t _{max} , ms; complex points	Measurement time, h	Relative sensitivity (peak pairs/ central peaks)			
Sequential backbone connective	vities (3D spectra)						
$\underline{\mathbf{H}}^{\alpha/\beta}\underline{\mathbf{C}}^{\alpha/\beta}(CO)\mathbf{NHN}$	$\omega_1(^{13}C^{\alpha/\beta}/^1H^{\alpha/\beta})$	6.3; 95	9.2	(0.56/0.34)			
(^{13}C)	$\omega_2(^{15}N)$	21.5; 28					
HACA(CO)NHN	$\omega_1(^{13}C^{\alpha/1}H^{\alpha})$	6.5; 54	5.4	(1.00 [‡] /0.81)			
(^{13}C)	$\omega_2(^{15}N)$	21.5; 28					
Intraresidual backbone connectivities (3D spectra)							
HNN <u>CAHA</u>	$\omega_1(^{13}C^{\alpha}/^1H^{\alpha})$	6.6; 51	5.0	(0.41/0.27)			
(INEPT)	$\omega_2(^{15}N)$	21.5; 28					
$\underline{\mathbf{H}}^{\alpha/\beta}\underline{\mathbf{C}}^{\alpha/\beta}\mathbf{COHA}$	$\omega_1(^{13}C^{\alpha/\beta}/^1H^{\alpha/\beta})$	6.3; 95	10.0	(0.22/0.11)			
(¹³ C)	$\omega_2(^{13}C==O)$	17.8; 32					
HNNCACB	$\omega_1(^{13}C^{\alpha/\beta})$	6.6; 56	8.0	(0.56)			
	ω ₂ (¹⁵ N)	21.5; 28					
Intra- and sequential-backbone connectivities (3D spectrum)							
HNN(<u>CO,CA</u>)	$\omega_1^{(13}C^{\alpha}/^{13}C=0)$	8.0/16.0 [§] ; 54	5.5	(0.54/1.41)			
(INEPT)	$\omega_2^{(15}N)$	21.5; 28					
Assignment of aliphatic resonances (3D spectra)							
HCCH-COSY	$\omega_1^{(13}\text{C/}^1\text{H})$	6.3; 95	6.2	(0.34/0.25)			
(^{13}C)	$\omega_2(^{13}\text{C})$	6.4; 20					
<u>HC</u> CH-TOCSY [¶]	$\omega_1(^{13}\text{C/}^1\text{H})$	6.3; 95	7.0	(0.19/n.d.)			
(^{13}C)	ω ₂ (¹³ C)	6.4; 20					

Assignment of aromatic resonances (2D spectra)							
HBCB(CGCD)HD	$\omega_1(^{13}\text{C}/^1\text{H})$	6.3; 95	5.3	(0.45/0.33)			
(¹³ C)	,						
¹ H-TOCSY- <u>HC</u> H-COSY [†]	$\omega_1(^{13}\text{C}/^1\text{H})$	15; 150	3.4	(0.76/-)			
H-10C31- <u>HC</u> H-C031	$w_{l}(C/H)$,		,			

One millimolar solution of "Z-domain" of Staphylococcal protein A at $T = 25^{\circ}$ C. The radio-frequency (rf) carrier for ¹H-frequency labeling in the projected "HC"-dimensions in which the chemical shifts of the aliphatic moieties are measured was set to 0 ppm. In 2D ¹H-TOCSY-HCH-COSY, the ¹H rf carrier was set to the position of the water line throughout. t_{max} denotes the maximal evolution time. The suite of experiments in this table can provide complete resonance assignments of proteins, excluding only the side chain NH_n moieties, the CH^e groups of histidinyl, and the CH^{e3}, CH^{e2,3}, and CHⁿ² groups of tryptophanyl residues (which can be obtained as described in ref. 17). Notably, Z-domain does not contain tryptophans.

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^{*} Approach 1: Use of incomplete polarization transfer (rows labeled with "INEPT"); Approach 2: use of ¹³C steady state magnetization (rows labeled with "¹³C").

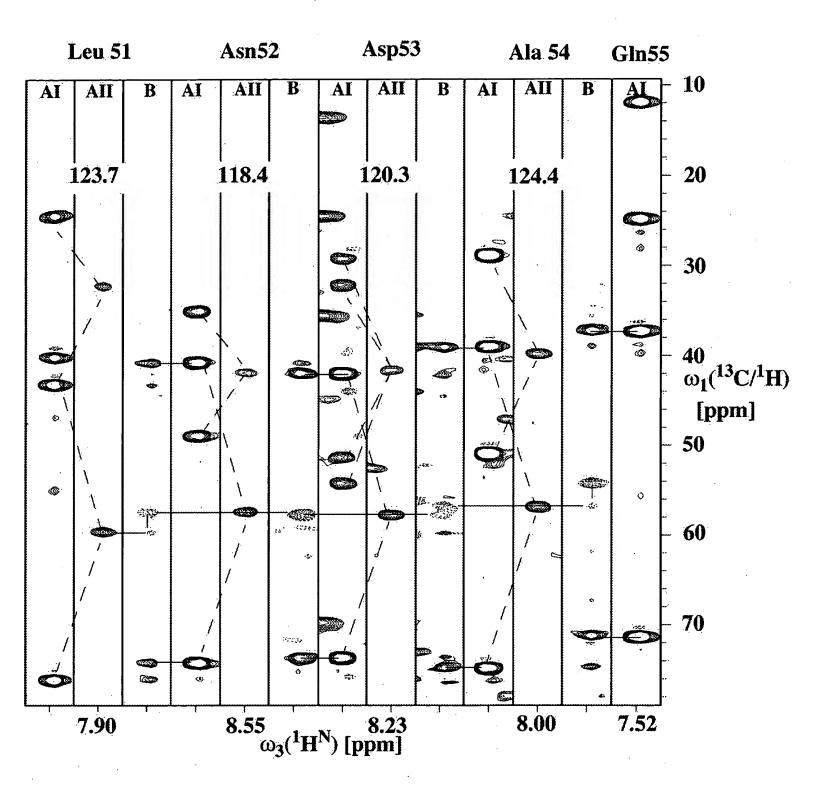
[†] Direct dimension: $t_{\text{max}} = 73 \text{ ms/}512 \text{ complex points.}$

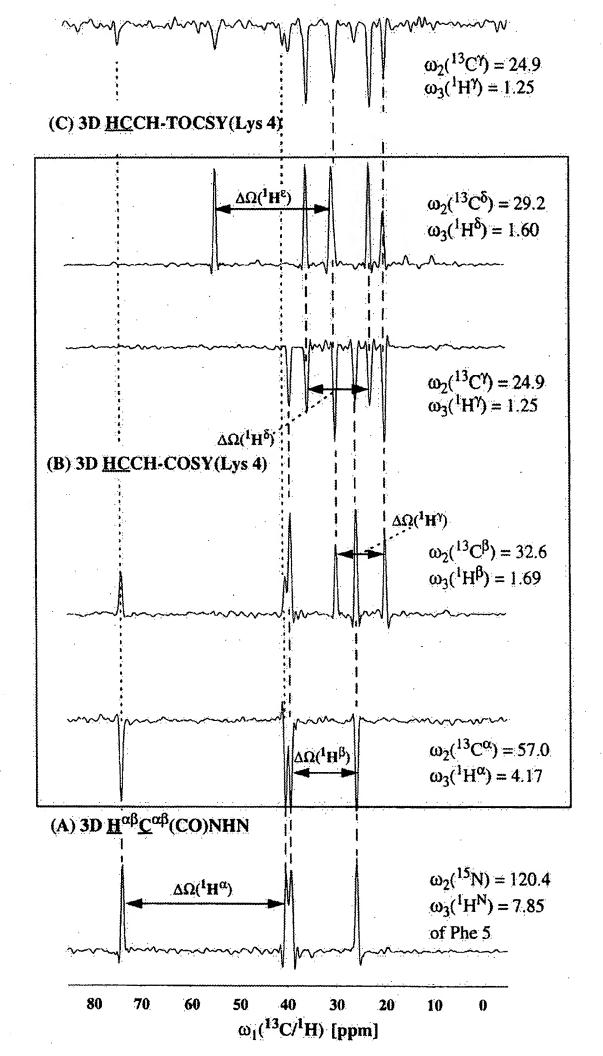
[‡] The average signal-to-noise (S/N) ratio of peaks observed in this subspectrum was 33.2.

[§] The increment for ${}^{13}C^{\alpha}$ chemical shift evolution was scaled by a factor of 0.5 relative to the values used to sample ${}^{13}C$ =O evolution (5).

[¶] The mixing times for the ¹³C-TOCSY relay was set to 21 ms. The S/N ratios for the double-relay central peaks were too low to be accurately evaluated.

^B The mixing time for the ¹H-TOCSY relay was set to 25 ms. The acquisition of central peaks is prevented by the use of spin-lock purge pulses (flanking the total correlation relay) to obtain pure phases.





2D ¹H-TOCSY-relayed <u>HC</u>H-COSY

